SEQUENCE LISTING

(1) GENERAL INFORMATION

(i) APPLICANT: BILLING-MEDEL, PATRICIA
                COHEN, MAURICE
                COLPITTS, TRACEY L.
                FRIEDMAN, PAULA N.
                KLASS, MICHAEL R.
                RUSSELL, JOHN C.
                STROUPE, STEPHEN D.

(ii) TITLE OF THE INVENTION: REAGENTS AND METHODS USEFUL
      FOR DETECTING DISEASES OF THE LUNG

(iii) NUMBER OF SEQUENCES: 20

(iv) CORRESPONDENCE ADDRESS:
   (A) ADDRESSEE: Abbott Laboratories
   (B) STREET: 100 Abbott Park Road
   (C) CITY: Abbott Park
   (D) STATE: IL
   (E) COUNTRY: USA
   (F) ZIP: 60064-3500

(v) COMPUTER READABLE FORM:
   (A) MEDIUM TYPE: Diskette
   (B) COMPUTER: IBM Compatible
   (C) OPERATING SYSTEM: DOS
   (D) SOFTWARE: FastSEQ for Windows Version 2.0

(vi) CURRENT APPLICATION DATA:
   (A) APPLICATION NUMBER:
   (B) FILING DATE:
   (C) CLASSIFICATION:

(vii) PRIOR APPLICATION DATA:
   (A) APPLICATION NUMBER: 60/048,810
   (B) FILING DATE: 05-JUN-1997

(viii) ATTORNEY/AGENT INFORMATION:
   (A) NAME: Becker, Cheryl L.
   (B) REGISTRATION NUMBER: 35,441
   (C) REFERENCE/DOCKET NUMBER: 6104.US.01

(ix) TELECOMMUNICATION INFORMATION:
   (A) TELEPHONE: 847/935-1729
   (B) TELEFAX: 847/938-2623
   (C) TELEX:

(2) INFORMATION FOR SEQ ID NO:1:

(i) SEQUENCE CHARACTERISTICS:
  (A) LENGTH: 239 base pairs
  (B) TYPE: nucleic acid
  (C) STRANDEDNESS: single
  (D) TOPOLOGY: linear

(ix) FEATURE:
  (A) NAME/KEY: base_polymorphism
  (B) LOCATION: 200
  (D) OTHER INFORMATION: /note= "'N' represents an A or G or
      T or C polymorphism at this position"

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1:

```
GGCCACCGGG ACTTCAGTGT CTCCTCCATC CCAGGAGCGC AGTGGCCACT ATGGGGTCTG    60
GGCTGCCCCT TGTCCTCCTC TTGACCCTCC TTGGCAGCTC ACATGGAACA GGGCCGGGTA   120
TGACTTTGCA ACTGAAGCTG AAGGAGTCTT TTCTGACAAA TTCCTCCTAT GAGTCCAGCT   180
TCCTGGAATT GCTTGAAAAN TCTGCCTCCT CCTCCATCTC CCTTCAGGGA CCAGCGTCA    239
```

(2) INFORMATION FOR SEQ ID NO:2:

(i) SEQUENCE CHARACTERISTICS:
  (A) LENGTH: 229 base pairs
  (B) TYPE: nucleic acid
  (C) STRANDEDNESS: single
  (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:2:

```
ACCGGGACTT CAGTGTCTCC TCCATCCCAG GAGCGCAGTG GCCACTATGG GGTCTGGGCT    60
GCCCCTTGTC CTCCTCTTGA CCCTCCTTGG CAGCTCACAT GGAACAGGGC CGGGTATGAC   120
TTTGCAACTG AAGCTGAAGG AGTCTTTTCT GACAAATTCC TCCTATGAGT CCAGCTTCCT   180
GGAATTGCTT GAAAAGTCTG CCTCCTCCTC CATCTCCCTT CAGGGACCA               229
```

(2) INFORMATION FOR SEQ ID NO:3:

(i) SEQUENCE CHARACTERISTICS:
  (A) LENGTH: 180 base pairs
  (B) TYPE: nucleic acid
  (C) STRANDEDNESS: single
  (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:3:

```
CAGGAGCGCA GTGGCCACTA TGGGGTCTGG GCTGCCCCTT GTCCTCCTCT TGACCCTCCT    60
TGGCAGCTCA CATGGAACAG GGCCGGGTAT GACTTTGCAA CTGAAGCTGA AGGAGTCTTT   120
TCTGACAAGT TCCTCCTATG AGTCCAGCTT CCTGGAATTG CTTGAAAAGC TCTGCCTCCT   180
```

(2) INFORMATION FOR SEQ ID NO:4:

(i) SEQUENCE CHARACTERISTICS:
  (A) LENGTH: 165 base pairs
  (B) TYPE: nucleic acid
  (C) STRANDEDNESS: single
  (D) TOPOLOGY: linear

(ix) FEATURE:
  (A) NAME/KEY: base_polymorphism
  (B) LOCATION: 68
  (D) OTHER INFORMATION: /note= "'N' represents an A or G or
      T or C polymorphism at this position"

```
(ix)    FEATURE:
        (A) NAME/KEY: base_polymorphism
        (B) LOCATION: 101
        (D) OTHER INFORMATION: /note= "'N' represents an A or G or
            T or C polymorphism at this position"

(ix)    FEATURE:
        (A) NAME/KEY: base_polymorphism
        (B) LOCATION: 124
        (D) OTHER INFORMATION: /note= "'N' represents an A or G or
            T or C polymorphism at this position"

(ix)    FEATURE:
        (A) NAME/KEY: base_polymorphism
        (B) LOCATION: 131
        (D) OTHER INFORMATION: /note= "'N' represents an A or G or
            T or C polymorphism at this position"
```

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:4:

```
TCAACACCAT GTTGTCTGCA ACACATGACA GCCATTGAAG CCTGTGTCCT TCTTGGCCCG      60
GGCTTTTNGG CGGGGAATGC AGGAGGCAGG CCCCGACCCT NTCTTTCAGC AGGCCCCCAC     120
CCTNCTGAGT NGCAATAAAT AAAATTCGGT ATGCTGAATT CAATA                     165
```

(2) INFORMATION FOR SEQ ID NO:5:

(i) SEQUENCE CHARACTERISTICS:
  (A) LENGTH: 389 base pairs
  (B) TYPE: nucleic acid
  (C) STRANDEDNESS: single
  (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:5:

```
CAGGAGCGCA GTGGCCACTA TGGGGTCTGG GCTGCCCCTT GTCCTCCTCT TGACCCTCCT      60
TGGCAGCTCA CATGGAACAG GGCCGGGTAT GACTTTGCAA CTGAAGCTGA AGGAGTCTTT     120
TCTGACAAGT TCCTCCTATG AGTCCAGCTT CCTGGAATTG CTTGAAAAGC TCTGCCTCCT     180
CCTCCATCTC CCTTCAGGGA CCAGCGTCAC CCTCCACCAT GCAAGATCTC AACACCATGT     240
TGTCTGCAAC ACATGACAGC CATTGAAGCC TGTGTCCTTC TTGGCCCGGG CTTTTGGGCC     300
GGGGATGCAG GAGGCAGGCC CCGACCCTGT CTTTCAGCAG GCCCCCACCC TCCTGAGTGG     360
CAATAAATAA AATTCGGTAT GCTGAATTC                                        389
```

(2) INFORMATION FOR SEQ ID NO:6:

(i) SEQUENCE CHARACTERISTICS:
  (A) LENGTH: 413 base pairs
  (B) TYPE: nucleic acid
  (C) STRANDEDNESS: single
  (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:6:

```
ACCGGGACTT CAGTGTCTCC TCCATCCCAG GAGCGCAGTG GCCACTATGG GGTCTGGGCT      60
GCCCCTTGTC CTCCTCTTGA CCCTCCTTGG CAGCTCACAT GGAACAGGGC CGGGTATGAC     120
TTTGCAACTG AAGCTGAAGG AGTCTTTTCT GACAAATTCC TCCTATGAGT CCAGCTTCCT     180
GGAATTGCTT GAAAAGCTCT GCCTCCTCCT CCATCTCCCT TCAGGGACCA GCGTCACCCT     240
CCACCATGCA AGATCTCAAC ACCATGTTGT CTGCAACACA TGACAGCCAT TGAAGCCTGT     300
GTCCTTCTTG GCCCGGGCTT TTGGGCCGGG GATGCAGGAG GCAGGCCCCG ACCCTGTCTT     360
TCAGCAGGCC CCCACCCTCC TGAGTGGCAA TAAATAAAAT TCGGTATGCT TGA            413
```

(2) INFORMATION FOR SEQ ID NO:7:

(i) SEQUENCE CHARACTERISTICS:

```
        (A) LENGTH: 424 base pairs
        (B) TYPE: nucleic acid
        (C) STRANDEDNESS: single
        (D) TOPOLOGY: linear


    (xi) SEQUENCE DESCRIPTION: SEQ ID NO:7:

GGCCACCGGG ACTTCAGTGT CTCCTCCATC CCAGGAGCGC AGTGGCCACT ATGGGGTCTG      60
GGCTGCCCCT TGTCCTCCTC TTGACCCTCC TTGGCAGCTC ACATGGAACA GGGCCGGGTA     120
TGACTTTGCA ACTGAAGCTG AAGGAGTCTT TTCTGACAAA TTCCTCCTAT GAGTCCAGCT     180
TCCTGGAATT GCTTGAAAAG CTCTGCCTCC TCCTCCATCT CCCTTCAGGG ACCAGCGTCA     240
CCCTCCACCA TGCAAGATCT CAACACCATG TTGTCTGCAA CACATGACAG CCATTGAAGC     300
CTGTGTCCTT CTTGGCCCGG GCTTTTGGGC CGGGGATGCA GGAGGCAGGC CCCGACCCTG     360
TCTTTCAGCA GGCCCCCACC CTCCTGAGTG GCAATAAATA AAATTCGGTA TGCTGAATTC     420
AATA                                                                 424

        (2) INFORMATION FOR SEQ ID NO:8:

    (i) SEQUENCE CHARACTERISTICS:
        (A) LENGTH: 68 base pairs
        (B) TYPE: nucleic acid
        (C) STRANDEDNESS: single
        (D) TOPOLOGY: linear


    (xi) SEQUENCE DESCRIPTION: SEQ ID NO:8:           '

AGCTCGGAAT TCCGAGCTTG GATCCTCTAG AGCGGCCGCC GACTAGTGAG CTCGTCGACC      60
CGGGAATT                                                              68

        (2) INFORMATION FOR SEQ ID NO:9:

    (i) SEQUENCE CHARACTERISTICS:
        (A) LENGTH: 68 base pairs
        (B) TYPE: nucleic acid
        (C) STRANDEDNESS: single
        (D) TOPOLOGY: linear


    (xi) SEQUENCE DESCRIPTION: SEQ ID NO:9:

AATTAATTCC CGGGTCGACG AGCTCACTAG TCGGCGGCCG CTCTAGAGGA TCCAAGCTCG      60
GAATTCCG                                                              68

        (2) INFORMATION FOR SEQ ID NO:10:

    (i) SEQUENCE CHARACTERISTICS:
        (A) LENGTH: 26 base pairs
        (B) TYPE: nucleic acid
        (C) STRANDEDNESS: single
        (D) TOPOLOGY: linear


    (xi) SEQUENCE DESCRIPTION: SEQ ID NO:10:

TTTTTTTTTT TTTTTTTTTT TTTTTC                                          26

        (2) INFORMATION FOR SEQ ID NO:11:

    (i) SEQUENCE CHARACTERISTICS:
        (A) LENGTH: 18 base pairs
        (B) TYPE: nucleic acid
        (C) STRANDEDNESS: single
        (D) TOPOLOGY: linear
```

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:11:

TGTAAAACGA CGGCCAGT   18

　　　(2) INFORMATION FOR SEQ ID NO:12:

　　　(i) SEQUENCE CHARACTERISTICS:
　　　　(A) LENGTH: 20 base pairs
　　　　(B) TYPE: nucleic acid
　　　　(C) STRANDEDNESS: single
　　　　(D) TOPOLOGY: linear

　　　(xi) SEQUENCE DESCRIPTION: SEQ ID NO:12:

AAGGACACAG GCTTCAATGG   20

　　　(2) INFORMATION FOR SEQ ID NO:13:

　　　(i) SEQUENCE CHARACTERISTICS:
　　　　(A) LENGTH: 32 base pairs
　　　　(B) TYPE: nucleic acid
　　　　(C) STRANDEDNESS: single
　　　　(D) TOPOLOGY: linear

　　　(xi) SEQUENCE DESCRIPTION: SEQ ID NO:13:

GCCGCCATGG ACCTGCTGCT GGACTCTTAT AG   32

　　　(2) INFORMATION FOR SEQ ID NO:14:

　　　(i) SEQUENCE CHARACTERISTICS:
　　　　(A) LENGTH: 30 base pairs
　　　　(B) TYPE: nucleic acid
　　　　(C) STRANDEDNESS: single
　　　　(D) TOPOLOGY: linear

　　　(xi) SEQUENCE DESCRIPTION: SEQ ID NO:14:

GCGGCCGCCC ACAATGATGT CATAGACACG   30

　　　(2) INFORMATION FOR SEQ ID NO:15:

　　　(i) SEQUENCE CHARACTERISTICS:
　　　　(A) LENGTH: 78 amino acids
　　　　(B) TYPE: amino acid
　　　　(C) STRANDEDNESS: single
　　　　(D) TOPOLOGY: linear

　　　(ii) MOLECULE TYPE: None

　　　(xi) SEQUENCE DESCRIPTION: SEQ ID NO:15:

Met Gly Ser Gly Leu Pro Leu Val Leu Leu Leu Thr Leu Leu Gly Ser
1   5   10   15
Ser His Gly Thr Gly Pro Gly Met Thr Leu Gln Leu Lys Leu Lys Glu
            20   25   30
Ser Phe Leu Thr Asn Ser Ser Tyr Glu Ser Ser Phe Leu Glu Leu Leu
        35   40   45
Glu Lys Leu Cys Leu Leu Leu His Leu Pro Ser Gly Thr Ser Val Thr
    50   55   60
Leu His His Ala Arg Ser Gln His His Val Val Cys Asn Thr
65   70   75

(2) INFORMATION FOR SEQ ID NO:16:

    (i) SEQUENCE CHARACTERISTICS:
      (A) LENGTH: 29 amino acids
      (B) TYPE: amino acid
      (C) STRANDEDNESS: single
      (D) TOPOLOGY: linear

    (ii) MOLECULE TYPE: None

    (xi) SEQUENCE DESCRIPTION: SEQ ID NO:16:

Ser Ser His Gly Thr Gly Pro Gly Met Thr Leu Gln Leu Lys Leu Lys
1   5   10   15
Glu Ser Phe Leu Thr Asn Ser Ser Tyr Glu Ser Ser Phe
            20   25

(2) INFORMATION FOR SEQ ID NO:17:

    (i) SEQUENCE CHARACTERISTICS:
      (A) LENGTH: 30 amino acids
      (B) TYPE: amino acid
      (C) STRANDEDNESS: single
      (D) TOPOLOGY: linear

    (ii) MOLECULE TYPE: None

    (xi) SEQUENCE DESCRIPTION: SEQ ID NO:17:

Glu Lys Leu Cys Leu Leu Leu His Leu Pro Ser Gly Thr Ser Val Thr
1   5   10   15
Leu His His Ala Arg Ser Gln His His Val Val Cys Asn Thr
            20   25   30

(2) INFORMATION FOR SEQ ID NO:18:

    (i) SEQUENCE CHARACTERISTICS:
      (A) LENGTH: 33 amino acids
      (B) TYPE: amino acid
      (C) STRANDEDNESS: single
      (D) TOPOLOGY: linear

    (ii) MOLECULE TYPE: None

    (xi) SEQUENCE DESCRIPTION: SEQ ID NO:18:

Glu Lys Ser Ala Ser Ser Ser Ile Ser Leu Gln Gly Pro Ala Ser Pro
1   5   10   15
Ser Thr Met Gln Asp Leu Asn Thr Met Leu Ser Ala Thr His Asp Ser
            20   25   30
His

(2) INFORMATION FOR SEQ ID NO:19:

    (i) SEQUENCE CHARACTERISTICS:
      (A) LENGTH: 8 amino acids
      (B) TYPE: amino acid
      (C) STRANDEDNESS: single
      (D) TOPOLOGY: linear

    (xi) SEQUENCE DESCRIPTION: SEQ ID NO:19:

```
Asp Tyr Lys Asp Asp Asp Asp Lys
1               5
```

(2) INFORMATION FOR SEQ ID NO:20:

    (i) SEQUENCE CHARACTERISTICS:
      (A) LENGTH: 21 amino acids
      (B) TYPE: amino acid
      (C) STRANDEDNESS: single
      (D) TOPOLOGY: linear

    (xi) SEQUENCE DESCRIPTION: SEQ ID NO:20:

```
Glu Gln Lys Leu Ile Ser Glu Glu Asp Leu Asn Met His Thr Glu His
1               5                   10                  15
His His His His His
              20
```